

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re: Tarczynski et al. Confirmation No.: To be assigned  
Appl. No.: To be assigned  
Filed: August 16, 2001  
For: METHODS AND COMPOSITIONS FOR MODIFYING OIL  
AND PROTEIN CONTENT IN PLANTS


**STATEMENT IN SUPPORT OF FILING A  
SEQUENCE LISTING UNDER 37 CFR § 1.821(f)**

Commissioner for Patents  
Washington, DC 20231

Sir:

I hereby state that the content of the paper and computer readable copies of the Sequence Listing, submitted concurrently herewith in accordance with 37 CFR § 1.821(c) and (e), are the same.

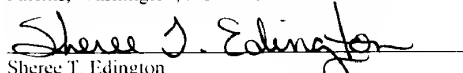
Respectfully submitted,

  
W. Murray Spruill  
Attorney for Applicant  
Registration No. 32,943

**Customer No. 00826**  
**Alston & Bird LLP**  
Bank of America Plaza  
101 South Tryon Street, Suite 4000  
Charlotte, NC 28280-4000  
Tel Raleigh Office (919) 862-2200  
Fax Raleigh Office (919) 862-2260

"Express Mail" Mailing Label Number EL 868638019 US  
Date of Deposit: August 16, 2001

I hereby certify that this paper or fee is being deposited with the United States Postal Service "Express Mail Post Office to Addressee" service under 37 CFR 1.10 on the date indicated above and is addressed to Box Patent Application, Commissioner for Patents, Washington, DC 20231.

  
Sheree T. Edington

# SEQUENCE LISTING

<110> Tarczynski, Mitchell C  
Li, Changjiang

<120> Methods and Compositions for Modifying Oil and Protein  
Content in Plants

<130> 5718-113 (35718/236392)

<140>

<141>

<150> 60/226,142

<151> 2000-08-18

<160> 6

<170> PatentIn Ver. 2.1

<210> 1

<211> 2245

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (138)..(1844)

<400> 1

cgaaaaccct cgcggcgagg agcgtctctc gtccacaca cgcgcgcgcg agcctccgca 60

gtccgcacct gctccacga cctgtcgtgc tcgtgcgcta ctctcctcga gcgcggcgcg 120

gagcacgggg acatcaa atg gcg gca gcg gcg gag atc ggt ggt ttc gcg 170  
Met Ala Ala Ala Ala Glu Ile Gly Gly Phe Ala  
1 5 10

gcg gcg aga gtg gcg gtg gca acg ctc agg ccg gct gcg cac cca gcc 218  
Ala Ala Arg Val Ala Val Ala Thr Leu Arg Pro Ala Ala His Pro Ala  
15 20 25

ccg gcg gcg gcg gcg gca ccg cag cct agg agg gcg gtg gcg gcg cag 266  
Pro Ala Ala Ala Ala Ala Pro Gln Pro Arg Arg Ala Val Ala Ala Gln  
30 35 40

tcg ctg cag acg acc gcc acc gag gcg ctg acg gcg gat ctc gcc gcc 314  
Ser Leu Gln Thr Thr Ala Thr Glu Ala Leu Thr Ala Asp Leu Ala Gly

45

50

55

acg acc aac ggc gct gtg cat gct cgg atg aat agt aag gct aca agt 362  
 Thr Thr Asn Gly Ala Val His Ala Arg Met Asn Ser Lys Ala Thr Ser  
 60 65 70 75

gaa atc act tca cag gca gtt act gca aat tct agg aga aag aca aag 410  
 Glu Ile Thr Ser Gln Ala Val Thr Ala Asn Ser Arg Arg Lys Thr Lys  
 80 85 90

ata gtc tgc acc ata ggt ccc tca acc aac act cgt gag atg att tgg 458  
 Ile Val Cys Thr Ile Gly Pro Ser Thr Asn Thr Arg Glu Met Ile Trp  
 95 100 105

aag ctt gca gag act gga atg aat gta gcg cgc ctt aat atg tcc cat 506  
 Lys Leu Ala Glu Thr Gly Met Asn Val Ala Arg Leu Asn Met Ser His  
 110 115 120

ggt gac cac cag tgc cac cag aag gtt att gat ttg gtc aag gag tac 554  
 Gly Asp His Gln Ser His Gln Lys Val Ile Asp Leu Val Lys Glu Tyr  
 125 130 135

aat gca cag aac act gat ggc aat gtt att gcc att atg ctg gac aca 602  
 Asn Ala Gln Asn Thr Asp Gly Asn Val Ile Ala Ile Met Leu Asp Thr  
 140 145 150 155

aag ggt cct gaa gtt aga agt ggg gat gtt cca gag cca atc atg ctc 650  
 Lys Gly Pro Glu Val Arg Ser Gly Asp Val Pro Glu Pro Ile Met Leu  
 160 165 170

aag gaa ggt caa gag ttc aac ttc acg att aaa aga ggg gtg agc act 698  
 Lys Glu Gly Gln Glu Phe Asn Phe Thr Ile Lys Arg Gly Val Ser Thr  
 175 180 185

gaa gac act gtc agc gtg aac tat gat gac ttc ata aat gat gtt gaa 746  
 Glu Asp Thr Val Ser Val Asn Tyr Asp Asp Phe Ile Asn Asp Val Glu  
 190 195 200

gct ggc gac ata cta tta gtg gat gga gga atg atg tgc ctt gct gtg 794  
 Ala Gly Asp Ile Leu Leu Val Asp Gly Gly Met Met Ser Leu Ala Val  
 205 210 215

aag tct aaa aca gcc gat aca gtc aag tgt aaa gta gtt gat ggt ggg 842  
 Lys Ser Lys Thr Ala Asp Thr Val Lys Cys Lys Val Val Asp Gly Gly  
 220 225 230 235

gaa ttg aaa tca cgg cgc cac cta aat gtc cgt gga aag agt gct act 890  
 Glu Leu Lys Ser Arg Arg His Leu Asn Val Arg Gly Lys Ser Ala Thr

240	245	250	
ttg cca tct atc act gag aag gat	tgg gaa gac ata aaa ttt ggt gtc	938	
Leu Pro Ser Ile Thr Glu Lys Asp	Trp Glu Asp Ile Lys Phe Gly Val		
255	260	265	
gaa aac ggt gtt gat ttc tat gca gtt tcc ttt gtg aag gat gcc aaa	986		
Glu Asn Gly Val Asp Phe Tyr Ala Val Ser Phe Val Lys Asp Ala Lys			
270	275	280	
gtt atc cat gaa tta aaa gac tac ctt aaa agt gct aat gcc gat ata	1034		
Val Ile His Glu Leu Lys Asp Tyr Leu Lys Ser Ala Asn Ala Asp Ile			
285	290	295	
cat gtc att cca aaa att gaa agt gca gat tca ata cca aac ctg cag	1082		
His Val Ile Pro Lys Ile Glu Ser Ala Asp Ser Ile Pro Asn Leu Gln			
300	305	310	
tcc att att gct gct tca gat ggg gca atg gtg gcg cgt gga gac ctt	1130		
Ser Ile Ile Ala Ala Ser Asp Gly Ala Met Val Ala Arg Gly Asp Leu			
320	325	330	
ggg gct gaa ctt ccg att gag gat gtt cct ttg cta cag gca gag att	1178		
Gly Ala Glu Leu Pro Ile Glu Asp Val Pro Leu Leu Gln Ala Glu Ile			
335	340	345	
gtc caa aca tgt cga agc atg gag aaa cca gtc att gtc gct aca aat	1226		
Val Gln Thr Cys Arg Ser Met Glu Lys Pro Val Ile Val Ala Thr Asn			
350	355	360	
atg ttg gaa agc atg att gac cat cct act ccc act agg gca gaa gtt	1274		
Met Leu Glu Ser Met Ile Asp His Pro Thr Pro Thr Arg Ala Glu Val			
365	370	375	
tct gac ata gct att gca gtt cgg gaa ggt gct gat gcc atc atg tta	1322		
Ser Asp Ile Ala Ile Ala Val Arg Glu Gly Ala Asp Ala Ile Met Leu			
380	385	390	
tct ggc gaa act gct cat gga aag tat cca cta aag gca gtc aag gtg	1370		
Ser Gly Glu Thr Ala His Gly Lys Tyr Pro Leu Lys Ala Val Lys Val			
400	405	410	
atg cac act gtg gca ctc aga aca gaa tcc agc ctt tat aac cca act	1418		
Met His Thr Val Ala Leu Arg Thr Glu Ser Ser Leu Tyr Asn Pro Thr			
415	420	425	
act tct cct agt ctt gtt gca tct gca cag ggt cta cag aat gag gac	1466		
Thr Ser Pro Ser Leu Val Ala Ser Ala Gln Gly Leu Gln Asn Glu Asp			

430	435	440	
ttc tcc gca agc cag cta agt aaa atg ttc gga tct cat gca acg atg			1514
Phe Ser Ala Ser Gln Leu Ser Lys Met Phe Gly Ser His Ala Thr Met			
445	450	455	
atg gcc aac acc ctt cgc aca cca atc att gta ttt aca cag aca ggc			1562
Met Ala Asn Thr Leu Arg Thr Pro Ile Ile Val Phe Thr Gln Thr Gly			
460	465	470	475
tcc atg gct gtc ctc ctg agc cac tat cgt ccc tcg tct aca cta ttt			1610
Ser Met Ala Val Leu Leu Ser His Tyr Arg Pro Ser Ser Thr Leu Phe			
480	485	490	
gca ttt aca aac gag gaa cga gtg aag caa cgg cta gca ctc tac cag			1658
Ala Phe Thr Asn Glu Glu Arg Val Lys Gln Arg Leu Ala Leu Tyr Gln			
495	500	505	
ggc gtc atc cct att cac atg cag ttc tct gac gac gca gaa gaa act			1706
Gly Val Ile Pro Ile His Met Gln Phe Ser Asp Asp Ala Glu Glu Thr			
510	515	520	
ttc tcc aga gca att agc agc ttg ctg aaa gca caa tat gtg aag aag			1754
Phe Ser Arg Ala Ile Ser Ser Leu Leu Lys Ala Gln Tyr Val Lys Lys			
525	530	535	
gga gac tac gtc act ctt gtt cag agc gga gtg act tca atc tgg aga			1802
Gly Asp Tyr Val Thr Leu Val Gln Ser Gly Val Thr Ser Ile Trp Arg			
540	545	550	555
gag gaa tcc act cac cac atc caa gtg agg aaa gtt cag gtc			1844
Glu Glu Ser Thr His His Ile Gln Val Arg Lys Val Gln Val			
560	565		
tgatgtgccg gtgggaattg gtcgtctgag aaattttgat agcgcgcct gatgtgttat			1904
catcattata tgtgtaattt tactgtttta ccaggagatt gctacgtcga gttatatgtt			1964
gtgtcgaatt cacgtgtagg ctctgaatct tgactgtgtt cgttcatttt cgcttgtttc			2024
acactgaagt gttataagct caactttact gcttttgttt tcttgtgaaa cttgagttta			2084
gtttcttggtt acaaaaggag ctagcactaa cagggtggtg agttttgtaa acggggcgag			2144
gactgttgag ttaaaactgt tgtaataatg atatcgttcc tgcaagacga cacatgcatg			2204
gccagaaggc caaagtcaaa aaaaaaaaaa aaaaaaaaaa a			2245

<210> 2  
 <211> 569  
 <212> PRT  
 <213> Zea mays

<400> 2

Met Ala Ala Ala Ala Glu Ile Gly Gly Phe Ala Ala Ala Arg Val Ala  
 1 5 10 15

Val Ala Thr Leu Arg Pro Ala Ala His Pro Ala Pro Ala Ala Ala Ala  
 20 25 30

Ala Pro Gln Pro Arg Arg Ala Val Ala Ala Gln Ser Leu Gln Thr Thr  
 35 40 45

Ala Thr Glu Ala Leu Thr Ala Asp Leu Ala Gly Thr Thr Asn Gly Ala  
 50 55 60

Val His Ala Arg Met Asn Ser Lys Ala Thr Ser Glu Ile Thr Ser Gln  
 65 70 75 80

Ala Val Thr Ala Asn Ser Arg Arg Lys Thr Lys Ile Val Cys Thr Ile  
 85 90 95

Gly Pro Ser Thr Asn Thr Arg Glu Met Ile Trp Lys Leu Ala Glu Thr  
 100 105 110

Gly Met Asn Val Ala Arg Leu Asn Met Ser His Gly Asp His Gln Ser  
 115 120 125

His Gln Lys Val Ile Asp Leu Val Lys Glu Tyr Asn Ala Gln Asn Thr  
 130 135 140

Asp Gly Asn Val Ile Ala Ile Met Leu Asp Thr Lys Gly Pro Glu Val  
 145 150 155 160

Arg Ser Gly Asp Val Pro Glu Pro Ile Met Leu Lys Glu Gly Gln Glu  
 165 170 175

Phe Asn Phe Thr Ile Lys Arg Gly Val Ser Thr Glu Asp Thr Val Ser  
 180 185 190

Val Asn Tyr Asp Asp Phe Ile Asn Asp Val Glu Ala Gly Asp Ile Leu  
 195 200 205

Leu Val Asp Gly Gly Met Met Ser Leu Ala Val Lys Ser Lys Thr Ala  
 210 215 220

Asp	Thr	Val	Lys	Cys	Lys	Val	Val	Asp	Gly	Gly	Glu	Leu	Lys	Ser	Arg	225	230	235	240
Arg	His	Leu	Asn	Val	Arg	Gly	Lys	Ser	Ala	Thr	Leu	Pro	Ser	Ile	Thr	245	250	255	
Glu	Lys	Asp	Trp	Glu	Asp	Ile	Lys	Phe	Gly	Val	Glu	Asn	Gly	Val	Asp	260	265	270	
Phe	Tyr	Ala	Val	Ser	Phe	Val	Lys	Asp	Ala	Lys	Val	Ile	His	Glu	Leu	275	280	285	
Lys	Asp	Tyr	Leu	Lys	Ser	Ala	Asn	Ala	Asp	Ile	His	Val	Ile	Pro	Lys	290	295	300	
Ile	Glu	Ser	Ala	Asp	Ser	Ile	Pro	Asn	Leu	Gln	Ser	Ile	Ile	Ala	Ala	305	310	315	320
Ser	Asp	Gly	Ala	Met	Val	Ala	Arg	Gly	Asp	Leu	Gly	Ala	Glu	Leu	Pro	325	330	335	
Ile	Glu	Asp	Val	Pro	Leu	Leu	Gln	Ala	Glu	Ile	Val	Gln	Thr	Cys	Arg	340	345	350	
Ser	Met	Glu	Lys	Pro	Val	Ile	Val	Ala	Thr	Asn	Met	Leu	Glu	Ser	Met	355	360	365	
Ile	Asp	His	Pro	Thr	Pro	Thr	Arg	Ala	Glu	Val	Ser	Asp	Ile	Ala	Ile	370	375	380	
Ala	Val	Arg	Glu	Gly	Ala	Asp	Ala	Ile	Met	Leu	Ser	Gly	Glu	Thr	Ala	385	390	395	400
His	Gly	Lys	Tyr	Pro	Leu	Lys	Ala	Val	Lys	Val	Met	His	Thr	Val	Ala	405	410	415	
Leu	Arg	Thr	Glu	Ser	Ser	Leu	Tyr	Asn	Pro	Thr	Thr	Ser	Pro	Ser	Leu	420	425	430	
Val	Ala	Ser	Ala	Gln	Gly	Leu	Gln	Asn	Glu	Asp	Phe	Ser	Ala	Ser	Gln	435	440	445	
Leu	Ser	Lys	Met	Phe	Gly	Ser	His	Ala	Thr	Met	Met	Ala	Asn	Thr	Leu	450	455	460	
Arg	Thr	Pro	Ile	Ile	Val	Phe	Thr	Gln	Thr	Gly	Ser	Met	Ala	Val	Leu	465	470	475	480

Leu Ser His Tyr Arg Pro Ser Ser Thr Leu Phe Ala Phe Thr Asn Glu  
 485 490 495  
 Glu Arg Val Lys Gln Arg Leu Ala Leu Tyr Gln Gly Val Ile Pro Ile  
 500 505 510  
 His Met Gln Phe Ser Asp Asp Ala Glu Glu Thr Phe Ser Arg Ala Ile  
 515 520 525  
 Ser Ser Leu Leu Lys Ala Gln Tyr Val Lys Lys Gly Asp Tyr Val Thr  
 530 535 540  
 Leu Val Gln Ser Gly Val Thr Ser Ile Trp Arg Glu Glu Ser Thr His  
 545 550 555 560  
 His Ile Gln Val Arg Lys Val Gln Val  
 565

<210> 3  
 <211> 1922  
 <212> DNA  
 <213> Zea mays

<220>  
 <221> CDS  
 <222> (148)..(1674)

<400> 3  
 cccggggaag aatccttctc gacgcgcgcc ccattcattc ttggagggca agaagaacgc 60  
 gcagtccaaa agcgaaacaa ggggaagggg cgaggcagcc aaacgaatcc cagcacctgc 120  
 ctctcctttg cttgcgcaga tctagcg atg gcg gcg ggc ggt gag ttg gcg tgg 174  
 Met Ala Ala Gly Gly Glu Leu Ala Trp  
 1 5  
 ggg gag gag ccc gtg gcg cgg cgc cgg cct aag acc aag atc gtc tgc 222  
 Gly Glu Glu Pro Val Ala Arg Arg Arg Pro Lys Thr Lys Ile Val Cys  
 10 15 20 25  
 acg ctc ggc cgg gcg tgg cga tcc gtc gag atg atc tgg cgc ctg ctg 270  
 Thr Leu Gly Pro Ala Ser Arg Ser Val Glu Met Ile Ser Arg Leu Leu  
 30 35 40  
 cgc gcc ggg atg tgc gtc gcg cgc ttc aac ttc tcc cat ggc tcc cac 318



Arg	Ala	Gly	Met	Cys	Val	Ala	Arg	Phe	Asn	Phe	Ser	His	Gly	Ser	His		
			45					50					55				
gag tac cac cag gag acg ctc gac aac ctg cac gcc gcc atg gag ctc 366																	
Glu	Tyr	His	Gln	Glu	Thr	Leu	Asp	Asn	Leu	His	Ala	Ala	Met	Glu	Leu		
		60					65				70						
acc ggg atc ctc tgc gcc gtt atg ctc gac acc aag ggt cca gag att 414																	
Thr	Gly	Ile	Leu	Cys	Ala	Val	Met	Leu	Asp	Thr	Lys	Gly	Pro	Glu	Ile		
		75				80					85						
aga act gga ttt ttg aaa gat ggg aag cct att caa ttg ata aaa ggc 462																	
Arg	Thr	Gly	Phe	Leu	Lys	Asp	Gly	Lys	Pro	Ile	Gln	Leu	Ile	Lys	Gly		
	90				95					100					105		
caa gaa atc aca att tct aca gac tat agc att cag ggt gat gag aaa 510																	
Gln	Glu	Ile	Thr	Ile	Ser	Thr	Asp	Tyr	Ser	Ile	Gln	Gly	Asp	Glu	Lys		
			110					115					120				
atg ata tca atg agc tac aag aag ctt gct gtt gat ctg aag cca ggc 558																	
Met	Ile	Ser	Met	Ser	Tyr	Lys	Lys	Leu	Ala	Val	Asp	Leu	Lys	Pro	Gly		
			125					130					135				
agt gtc ata ttg tgt gct gat ggt acc atc act ctt act gtt ctt cac 606																	
Ser	Val	Ile	Leu	Cys	Ala	Asp	Gly	Thr	Ile	Thr	Leu	Thr	Val	Leu	His		
		140				145					150						
tgt gat aaa gaa caa ggc ttg gtt cgc tgc cgc tgt gag aac act ttc 654																	
Cys	Asp	Lys	Glu	Gln	Gly	Leu	Val	Arg	Cys	Arg	Cys	Glu	Asn	Thr	Phe		
	155					160					165						
aag ctt ggc gag agg aag aat gtt aat ctt cca gga gtt att gtt gat 702																	
Lys	Leu	Gly	Glu	Arg	Lys	Asn	Val	Asn	Leu	Pro	Gly	Val	Ile	Val	Asp		
	170				175					180					185		
ctc ccc aca ctc aca gac aag gac aag gag gac atc ctt aaa tgg ggt 750																	
Leu	Pro	Thr	Leu	Thr	Asp	Lys	Asp	Lys	Glu	Asp	Ile	Leu	Lys	Trp	Gly		
			190					195					200				
gtt cca aac aag att gac atg att gcc ttg tca ttt gtt cgg aag ggt 798																	
Val	Pro	Asn	Lys	Ile	Asp	Met	Ile	Ala	Leu	Ser	Phe	Val	Arg	Lys	Gly		
			205					210					215				
tcg gat ctt gtg gag gtt agg aag gta ctt ggt gag cat gcc aag tcc 846																	
Ser	Asp	Leu	Val	Glu	Val	Arg	Lys	Val	Leu	Gly	Glu	His	Ala	Lys	Ser		
		220				225					230						
ata atg ctg atg tca aag gtt gag aat caa gag gga gta gct aac ttt 894																	

Ile Met Leu Met Ser Lys Val Glu Asn Gln Glu Gly Val Ala Asn Phe	
235 240 245	
gat gat atc ctg gca aac tct gat gct ttt atg gtg gca aga ggt gat	942
Asp Asp Ile Leu Ala Asn Ser Asp Ala Phe Met Val Ala Arg Gly Asp	
250 255 260 265	
tta gga atg gaa att cct ata gag aag att ttc ttt gca cag aag gtg	990
Leu Gly Met Glu Ile Pro Ile Glu Lys Ile Phe Phe Ala Gln Lys Val	
270 275 280	
atg att ttc aag tgc aat att caa ggc aag cct gtt gtg act gca acc	1038
Met Ile Phe Lys Cys Asn Ile Gln Gly Lys Pro Val Val Thr Ala Thr	
285 290 295	
cag atg ttg gaa tct atg atc aag tct cct cgc cct act cgg gca gaa	1086
Gln Met Leu Glu Ser Met Ile Lys Ser Pro Arg Pro Thr Arg Ala Glu	
300 305 310	
gca acg gat gtt gca aac gca gtt ctt gat ggc aca gac tgt gtt atg	1134
Ala Thr Asp Val Ala Asn Ala Val Leu Asp Gly Thr Asp Cys Val Met	
315 320 325	
ctc agt ggt gag act gct gct ggg gct tat cca ggg ttg gcg gtg cag	1182
Leu Ser Gly Glu Thr Ala Ala Gly Ala Tyr Pro Gly Leu Ala Val Gln	
330 335 340 345	
act atg gct aag atc tgc ctg caa gca gag tct tgc gta gac cat gct	1230
Thr Met Ala Lys Ile Cys Leu Gln Ala Glu Ser Cys Val Asp His Ala	
350 355 360	
gct att ttc aaa tca atc atg gct tca gct cca att cca atg agt cca	1278
Ala Ile Phe Lys Ser Ile Met Ala Ser Ala Pro Ile Pro Met Ser Pro	
365 370 375	
ttg gag agc ctt gca tca tca gct gtt cgc aca gca aac tct gcc agg	1326
Leu Glu Ser Leu Ala Ser Ser Ala Val Arg Thr Ala Asn Ser Ala Arg	
380 385 390	
gca gca ctt atc ttg gtc ctg acc agg gga gga act act gct agg ctt	1374
Ala Ala Leu Ile Leu Val Leu Thr Arg Gly Gly Thr Thr Ala Arg Leu	
395 400 405	
gta gcc aag tat agg cca tcc atg ccg att ctg tcc gtt gtg gtt cct	1422
Val Ala Lys Tyr Arg Pro Ser Met Pro Ile Leu Ser Val Val Val Pro	
410 415 420 425	
gag ctg aag aca gac tcg ttc gac tgg gcc tgc agt gac gag ggt ccg	1470

Glu Leu Lys Thr Asp Ser Phe Asp Trp Ala Cys Ser Asp Glu Gly Pro  
 430 435 440  
 gca agg cac agc ctc att gtg agg ggt gtc atc cca atg ctg agt gcc 1518  
 Ala Arg His Ser Leu Ile Val Arg Gly Val Ile Pro Met Leu Ser Ala  
 445 450 455  
 gcc act gcc aag gcc ttt gac aac gaa gcc act gac gaa gct att ggt 1566  
 Ala Thr Ala Lys Ala Phe Asp Asn Glu Ala Thr Asp Glu Ala Ile Gly  
 460 465 470  
 ttt gcc att gaa aat gcg aag acg atg ggg cta tgc aac acc ggt caa 1614  
 Phe Ala Ile Glu Asn Ala Lys Thr Met Gly Leu Cys Asn Thr Gly Gln  
 475 480 485  
 tcc gtt gtg gcc ctg cac cgc atc ggg att tca tcc gtc atc aag ctt 1662  
 Ser Val Val Ala Leu His Arg Ile Gly Ile Ser Ser Val Ile Lys Leu  
 490 495 500 505  
 ctt act gtg aag taggggtcca aggggtgaggg acaccatttt gcttggtgaa 1714  
 Leu Thr Val Lys  
 tttttgtgag gctgcttaacg cacatcagcg tatccacagc ttttctgttg ccaaagatac 1774  
 agactttgcg ttctgggtaca ccttgggtgtt acaaggttgt gggaatttgt cgtttagata 1834  
 ttagcgattt aaacagttta tcaactgcta tagctaatta atttgcagct gtgctgcaac 1894  
 tttatcgtac tgaaaaaaaa aaaaaaaaaa 1922

<210> 4  
 <211> 509  
 <212> PRT  
 <213> Zea mays

<400> 4  
 Met Ala Ala Gly Gly Glu Leu Ala Trp Gly Glu Glu Pro Val Ala Arg  
 1 5 10 15  
 Arg Arg Pro Lys Thr Lys Ile Val Cys Thr Leu Gly Pro Ala Ser Arg  
 20 25 30  
 Ser Val Glu Met Ile Ser Arg Leu Leu Arg Ala Gly Met Cys Val Ala  
 35 40 45  
 Arg Phe Asn Phe Ser His Gly Ser His Glu Tyr His Gln Glu Thr Leu  
 50 55 60

Asp	Asn	Leu	His	Ala	Ala	Met	Glu	Leu	Thr	Gly	Ile	Leu	Cys	Ala	Val	65	70	75	80
Met	Leu	Asp	Thr	Lys	Gly	Pro	Glu	Ile	Arg	Thr	Gly	Phe	Leu	Lys	Asp	85	90	95	
Gly	Lys	Pro	Ile	Gln	Leu	Ile	Lys	Gly	Gln	Glu	Ile	Thr	Ile	Ser	Thr	100	105	110	
Asp	Tyr	Ser	Ile	Gln	Gly	Asp	Glu	Lys	Met	Ile	Ser	Met	Ser	Tyr	Lys	115	120	125	
Lys	Leu	Ala	Val	Asp	Leu	Lys	Pro	Gly	Ser	Val	Ile	Leu	Cys	Ala	Asp	130	135	140	
Gly	Thr	Ile	Thr	Leu	Thr	Val	Leu	His	Cys	Asp	Lys	Glu	Gln	Gly	Leu	145	150	155	160
Val	Arg	Cys	Arg	Cys	Glu	Asn	Thr	Phe	Lys	Leu	Gly	Glu	Arg	Lys	Asn	165	170	175	
Val	Asn	Leu	Pro	Gly	Val	Ile	Val	Asp	Leu	Pro	Thr	Leu	Thr	Asp	Lys	180	185	190	
Asp	Lys	Glu	Asp	Ile	Leu	Lys	Trp	Gly	Val	Pro	Asn	Lys	Ile	Asp	Met	195	200	205	
Ile	Ala	Leu	Ser	Phe	Val	Arg	Lys	Gly	Ser	Asp	Leu	Val	Glu	Val	Arg	210	215	220	
Lys	Val	Leu	Gly	Glu	His	Ala	Lys	Ser	Ile	Met	Leu	Met	Ser	Lys	Val	225	230	235	240
Glu	Asn	Gln	Glu	Gly	Val	Ala	Asn	Phe	Asp	Asp	Ile	Leu	Ala	Asn	Ser	245	250	255	
Asp	Ala	Phe	Met	Val	Ala	Arg	Gly	Asp	Leu	Gly	Met	Glu	Ile	Pro	Ile	260	265	270	
Glu	Lys	Ile	Phe	Phe	Ala	Gln	Lys	Val	Met	Ile	Phe	Lys	Cys	Asn	Ile	275	280	285	
Gln	Gly	Lys	Pro	Val	Val	Thr	Ala	Thr	Gln	Met	Leu	Glu	Ser	Met	Ile	290	295	300	
Lys	Ser	Pro	Arg	Pro	Thr	Arg	Ala	Glu	Ala	Thr	Asp	Val	Ala	Asn	Ala	305	310	315	320

Val Leu Asp Gly Thr Asp Cys Val Met Leu Ser Gly Glu Thr Ala Ala  
 325 330 335  
 Gly Ala Tyr Pro Gly Leu Ala Val Gln Thr Met Ala Lys Ile Cys Leu  
 340 345 350  
 Gln Ala Glu Ser Cys Val Asp His Ala Ala Ile Phe Lys Ser Ile Met  
 355 360 365  
 Ala Ser Ala Pro Ile Pro Met Ser Pro Leu Glu Ser Leu Ala Ser Ser  
 370 375 380  
 Ala Val Arg Thr Ala Asn Ser Ala Arg Ala Ala Leu Ile Leu Val Leu  
 385 390 395 400  
 Thr Arg Gly Gly Thr Thr Ala Arg Leu Val Ala Lys Tyr Arg Pro Ser  
 405 410 415  
 Met Pro Ile Leu Ser Val Val Val Pro Glu Leu Lys Thr Asp Ser Phe  
 420 425 430  
 Asp Trp Ala Cys Ser Asp Glu Gly Pro Ala Arg His Ser Leu Ile Val  
 435 440 445  
 Arg Gly Val Ile Pro Met Leu Ser Ala Ala Thr Ala Lys Ala Phe Asp  
 450 455 460  
 Asn Glu Ala Thr Asp Glu Ala Ile Gly Phe Ala Ile Glu Asn Ala Lys  
 465 470 475 480  
 Thr Met Gly Leu Cys Asn Thr Gly Gln Ser Val Val Ala Leu His Arg  
 485 490 495  
 Ile Gly Ile Ser Ser Val Ile Lys Leu Leu Thr Val Lys  
 500 505

<210> 5

<211> 2075

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (198)..(1736)

<400> 5

gogcccacgg aatcgcaatt cccactccc accccccttc tcttttctat aaagggaac 60  
ttcgccacca aatctcgaat cccatctcgc tgetctccgc cgetcgacgc cgacgccgac 120  
gocgacacct ctccctcccc cattccccgt gcccggacc goggagcaga cagaggcgag 180  
atccggagcg ccgcgcg atg gcg aac atc gac atg gcg aag atc ctg gcg 230  
Met Ala Asn Ile Asp Met Ala Lys Ile Leu Ala  
1 5 10  
gac ctg gac cgc gcc gcc gcc gac gcg cgg ctg ccc aag acc aag ctc 278  
Asp Leu Asp Arg Gly Ala Gly Asp Ala Arg Leu Pro Lys Thr Lys Leu  
15 20 25  
gtc tgc acg ctt gcc ccg gcc tcc cgc tcc gtg ccc atg ctc gag aag 326  
Val Cys Thr Leu Gly Pro Ala Ser Arg Ser Val Pro Met Leu Glu Lys  
30 35 40  
ctg ctc cgc gcc gcc atg aac gtc gcg cgc ttc aac ttc tcc cac gcc 374  
Leu Leu Arg Ala Gly Met Asn Val Ala Arg Phe Asn Phe Ser His Gly  
45 50 55  
acc cac cag tac cac cag gag acg ctc gac agc ctc cgc cag gcc atg 422  
Thr His Gln Tyr His Gln Glu Thr Leu Asp Ser Leu Arg Gln Ala Met  
60 65 70 75  
cac aac acc gcc atc ctc tgc gcc gtc atg ctc gac acc aag ggt cct 470  
His Asn Thr Gly Ile Leu Cys Ala Val Met Leu Asp Thr Lys Gly Pro  
80 85 90  
gag att cgt aca ggg ttt ttg aag gat ggt aaa cca att aag cta acc 518  
Glu Ile Arg Thr Gly Phe Leu Lys Asp Gly Lys Pro Ile Lys Leu Thr  
95 100 105  
aag ggt caa gag atc act gtt acc act gat tat gat atc aag ggt gac 566  
Lys Gly Gln Glu Ile Thr Val Thr Thr Asp Tyr Asp Ile Lys Gly Asp  
110 115 120  
gaa aaa atg atc gct atg agt tac aag aaa ctg cct gtt gac gtg aag 614  
Glu Lys Met Ile Ala Met Ser Tyr Lys Lys Leu Pro Val Asp Val Lys  
125 130 135  
cct gga aat gtc ata ctc tgc gca gat ggt act atc tct ctg gcc gtt 662  
Pro Gly Asn Val Ile Leu Cys Ala Asp Gly Thr Ile Ser Leu Ala Val  
140 145 150 155  
ctg tct tgc gat cct gat gct gga act gtg cgt tgt agg tgt gag aac 710

Leu Ser Cys Asp Pro Asp Ala Gly Thr Val Arg Cys Arg Cys Glu Asn	
160 165 170	
act gca atg ctt ggt gag aga aag aac tgc aat ttg cca gga att gtt	758
Thr Ala Met Leu Gly Glu Arg Lys Asn Cys Asn Leu Pro Gly Ile Val	
175 180 185	
gtg gat ctt cct aca ttg act gag aaa gat aaa gaa gat att ttg ggc	806
Val Asp Leu Pro Thr Leu Thr Glu Lys Asp Lys Glu Asp Ile Leu Gly	
190 195 200	
tgg ggt gtt cca aat gac att gac atg att gct cta tcc ttt gtc cgt	854
Trp Gly Val Pro Asn Asp Ile Asp Met Ile Ala Leu Ser Phe Val Arg	
205 210 215	
aaa gga tca gat ttg gtg act gtc aga cag gtt ctt ggg cag cat gcc	902
Lys Gly Ser Asp Leu Val Thr Val Arg Gln Val Leu Gly Gln His Ala	
220 225 230 235	
aag cgc att aag ttg atg tca aag gtt gag aac caa gag ggt gtt gta	950
Lys Arg Ile Lys Leu Met Ser Lys Val Glu Asn Gln Glu Gly Val Val	
240 245 250	
aac ttt gat gag atc ttg agg gag act gat gct ttt atg gtt gct aga	998
Asn Phe Asp Glu Ile Leu Arg Glu Thr Asp Ala Phe Met Val Ala Arg	
255 260 265	
ggt gat ctg gga atg gag att cca gtc gag aag att ttc ctt gcg cag	1046
Gly Asp Leu Gly Met Glu Ile Pro Val Glu Lys Ile Phe Leu Ala Gln	
270 275 280	
aag atg atg atc tac aag tgc aac att gct ggc aaa cct gtt gtt act	1094
Lys Met Met Ile Tyr Lys Cys Asn Ile Ala Gly Lys Pro Val Val Thr	
285 290 295	
gct acc cag atg ctc gag tcg atg atc aaa tct cct cgg ccg aca cgt	1142
Ala Thr Gln Met Leu Glu Ser Met Ile Lys Ser Pro Arg Pro Thr Arg	
300 305 310 315	
gct gag gcc act gac gtt gca aat gcc gtt ctt gat gga act gac tgt	1190
Ala Glu Ala Thr Asp Val Ala Asn Ala Val Leu Asp Gly Thr Asp Cys	
320 325 330	
gtc atg ctc agc gga gag agt gcc gct gga gcc tac ccc gag gtg gct	1238
Val Met Leu Ser Gly Glu Ser Ala Ala Gly Ala Tyr Pro Glu Val Ala	
335 340 345	
gtg aag atc atg gct cgt att tgc atc gag gca gaa tct tcc ctg gac	1286

Val Lys Ile Met Ala Arg Ile Cys Ile Glu Ala Glu Ser Ser Leu Asp  
 350 355 360

cac gag gca gtt ttc aag gcc atg atc agg tcc gcg cct ctt cca atg 1334  
 His Glu Ala Val Phe Lys Ala Met Ile Arg Ser Ala Pro Leu Pro Met  
 365 370 375

agc cct ctg gag tcc ctt gca tca tct gct gtg agg act gcc aac aag 1382  
 Ser Pro Leu Glu Ser Leu Ala Ser Ser Ala Val Arg Thr Ala Asn Lys  
 380 385 390 395

gcc aag gct gca ctg att gtc gtc ctg act cgc ggt ggc acc acg gcc 1430  
 Ala Lys Ala Ala Leu Ile Val Val Leu Thr Arg Gly Gly Thr Thr Ala  
 400 405 410

aaa ctg gtc gcc aag tac cgc ccc agg gtc ccc atc ctc tcc gtt gtc 1478  
 Lys Leu Val Ala Lys Tyr Arg Pro Arg Val Pro Ile Leu Ser Val Val  
 415 420 425

gta ccc gtg ctt acg acc gac tct ttc gac tgg acc atc agc tcc gag 1526  
 Val Pro Val Leu Thr Thr Asp Ser Phe Asp Trp Thr Ile Ser Ser Glu  
 430 435 440

ggc cca gct agg cac agc ctg atc tac aga ggc ctc att ccc ctc ctc 1574  
 Gly Pro Ala Arg His Ser Leu Ile Tyr Arg Gly Leu Ile Pro Leu Leu  
 445 450 455

gcc gag ggc tcc gcg aag gct acg gat tca gag tcg acg gag gtg atc 1622  
 Ala Glu Gly Ser Ala Lys Ala Thr Asp Ser Glu Ser Thr Glu Val Ile  
 460 465 470 475

ctt gag gcc gcg ttg aag tcg gcc gtg cag aag cag ctc tgc aag cct 1670  
 Leu Glu Ala Ala Leu Lys Ser Ala Val Gln Lys Gln Leu Cys Lys Pro  
 480 485 490

ggt gat gcc atc gtg gct ctt cat cgt att ggc gtc gcc tcc gtc atc 1718  
 Gly Asp Ala Ile Val Ala Leu His Arg Ile Gly Val Ala Ser Val Ile  
 495 500 505

aag atc tgc atc gtg aag tgatcaccac gacctgggttc tcaactgctgg 1766  
 Lys Ile Cys Ile Val Lys  
 510

gattccatga aacagctttt ctgcctcctt tttactgcat ttttttccgg agacagatat 1826

ttatgttgta agcctgcgtc tggtgtttgc agttgcggaa tgttttttgt tcacgtagtt 1886

atttagctgg taaatgggga gggagaggac tccattgatg ttagtggttaa taagatttgt 1946



gtctatggag ttgagttgaa aggggtttttt catgctaagc cccgagacac taggagatgg 2006  
 agatcgaggt tgagatgaga taagcaataa gtgaaaaaaaa tgttgatttg caaaaaaaaaa 2066  
 aaaaaaaaaa 2075

<210> 6  
 <211> 513  
 <212> PRT  
 <213> Zea mays

<400> 6

Met Ala Asn Ile Asp Met Ala Lys Ile Leu Ala Asp Leu Asp Arg Gly  
 1 5 10 15

Ala Gly Asp Ala Arg Leu Pro Lys Thr Lys Leu Val Cys Thr Leu Gly  
 20 25 30

Pro Ala Ser Arg Ser Val Pro Met Leu Glu Lys Leu Leu Arg Ala Gly  
 35 40 45

Met Asn Val Ala Arg Phe Asn Phe Ser His Gly Thr His Gln Tyr His  
 50 55 60

Gln Glu Thr Leu Asp Ser Leu Arg Gln Ala Met His Asn Thr Gly Ile  
 65 70 75 80

Leu Cys Ala Val Met Leu Asp Thr Lys Gly Pro Glu Ile Arg Thr Gly  
 85 90 95

Phe Leu Lys Asp Gly Lys Pro Ile Lys Leu Thr Lys Gly Gln Glu Ile  
 100 105 110

Thr Val Thr Thr Asp Tyr Asp Ile Lys Gly Asp Glu Lys Met Ile Ala  
 115 120 125

Met Ser Tyr Lys Lys Leu Pro Val Asp Val Lys Pro Gly Asn Val Ile  
 130 135 140

Leu Cys Ala Asp Gly Thr Ile Ser Leu Ala Val Leu Ser Cys Asp Pro  
 145 150 155 160

Asp Ala Gly Thr Val Arg Cys Arg Cys Glu Asn Thr Ala Met Leu Gly  
 165 170 175

Glu Arg Lys Asn Cys Asn Leu Pro Gly Ile Val Val Asp Leu Pro Thr



435

440

445

Ser Leu Ile Tyr Arg Gly Leu Ile Pro Leu Leu Ala Glu Gly Ser Ala  
450 455 460

Lys Ala Thr Asp Ser Glu Ser Thr Glu Val Ile Leu Glu Ala Ala Leu  
465 470 475 480

Lys Ser Ala Val Gln Lys Gln Leu Cys Lys Pro Gly Asp Ala Ile Val  
485 490 495

Ala Leu His Arg Ile Gly Val Ala Ser Val Ile Lys Ile Cys Ile Val  
500 505 510

Lys